Ti Worrall

TEAM 1
Paper # 312

INPUT SET: S29634.raw

> **This Raw Listing contains the General Information Section and up to the first 5 pages.**

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 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Radosevich, James A.
 6
 7       (ii) TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR
 8              CANCER
 9
10      (iii) NUMBER OF SEQUENCES: 9
11
12       (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
14              (B) STREET: NBC Tower - Suite 3600, 455 N. Cityfront
15                     Plaza Drive
16              (C) CITY: Chicago
17              (D) STATE: Illinois
18              (E) COUNTRY: USA
19              (F) ZIP: 60611-5599
20
21        (v) COMPUTER READABLE FORM:
22              (A) MEDIUM TYPE: Floppy disk
23              (B) COMPUTER: IBM PC compatible
24              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27       (vi) CURRENT APPLICATION DATA:
28              (A) APPLICATION NUMBER: US 09/040,485
29              (B) FILING DATE: 17-MAR-1998
30              (C) CLASSIFICATION:
31
32     (viii) ATTORNEY/AGENT INFORMATION:
33              (A) NAME: Martin, Alice O.
34              (B) REGISTRATION NUMBER: 35,601
35              (C) REFERENCE/DOCKET NUMBER: 8998/3
36
37       (ix) TELECOMMUNICATION INFORMATION:
38              (A) TELEPHONE: 312-321-4200
39              (B) TELEFAX: 312-321-4299
40
41
42   (2) INFORMATION FOR SEQ ID NO:1:
43
44        (i) SEQUENCE CHARACTERISTICS:
45              (A) LENGTH: 2442 base pairs
46              (B) TYPE: nucleic acid
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47              (C) STRANDEDNESS: single
48              (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: cDNA
51
52
53      (ix) FEATURE:
54              (A) NAME/KEY: CDS
55              (B) LOCATION: 70..834
56
57
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60  CGGGAGCTTG AAGGACACAA GAATGGGAGG AAAGGCGGAC TCTCAGGAAC TTCATTCTTC      60
61
62  ACGTGGTTT ATG GTG ATT GCA TTG CTG GGC GTC TGG ACA TCT GTA GCT         108
63            Met Val Ile Ala Leu Leu Gly Val Trp Thr Ser Val Ala
64             1               5                   10
65
66  GTC GTT TGG TTT GAT CTT GTT GAC TAT GAG GAA GTT CTA GGA AAA CTA       156
67  Val Val Trp Phe Asp Leu Val Asp Tyr Glu Glu Val Leu Gly Lys Leu
68       15              20                  25
69
70  GGA ATC TAT GAT GCT GAT GGT GAT GGA GAT TTT GAT GTG GAT GAT GCC       204
71  Gly Ile Tyr Asp Ala Asp Gly Asp Gly Asp Phe Asp Val Asp Asp Ala
72   30              35                  40                  45
73
74  AAA GTT TTA TTA GGA CTT AAA GAG AGA TCT ACT TCA GAG CCA GCA GTC       252
75  Lys Val Leu Leu Gly Leu Lys Glu Arg Ser Thr Ser Glu Pro Ala Val
76               50                  55                  60
77
78  CCG CCA GAA GAG GCT GAG CCA CAC ACT GAG CCC GAG GAG CAG GTT CCT       300
79  Pro Pro Glu Glu Ala Glu Pro His Thr Glu Pro Glu Glu Gln Val Pro
80               65                  70                  75
81
82  GTG GAG GCA GAA CCC CAG AAT ATC GAA GAT GAA GCA AAA GAA CAA ATT       348
83  Val Glu Ala Glu Pro Gln Asn Ile Glu Asp Glu Ala Lys Glu Gln Ile
84               80                  85                  90
85
86  CAG TCC CTT CTC CAT GAA ATG GTA CAC GCA GAA CAT GTT GAG GGA GAA       396
87  Gln Ser Leu Leu His Glu Met Val His Ala Glu His Val Glu Gly Glu
88        95                  100                 105
89
90  GAC TTG CAA CAA GAA GAT GGA CCC ACA GGA GAA CCA CAA CAA GAG GAT       444
91  Asp Leu Gln Gln Glu Asp Gly Pro Thr Gly Glu Pro Gln Gln Glu Asp
92  110                 115                 120                 125
93
94  GAT GAG TTT CTT ATG GCG ACT GAT GTA GAT GAT AGA TTT GAG ACC CTG       492
95  Asp Glu Phe Leu Met Ala Thr Asp Val Asp Asp Arg Phe Glu Thr Leu
96                   130                 135                 140
97
98  GAA CCT GAA GTA TCT CAT GAA GAA ACC GAG CAT AGT TAC CAC GTG GAA       540
99  Glu Pro Glu Val Ser His Glu Glu Thr Glu His Ser Tyr His Val Glu
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100                 145                 150                 155
101
102  GAG ACA GTT TCA CAA GAC TGT AAT CAG GAT ATG GAA GAG ATG ATG TCT      588
103  Glu Thr Val Ser Gln Asp Cys Asn Gln Asp Met Glu Glu Met Met Ser
104          160                 165                 170
105
106  GAG CAG GAA AAT CCA GAT TCC AGT GAA CCA GTA GTA GAA GAT GAA AGA      636
107  Glu Gln Glu Asn Pro Asp Ser Ser Glu Pro Val Val Glu Asp Glu Arg
108         175                 180                 185
109
110  TTG CAC CAT GAT ACA GAT GAT GTA ACA TAC CAA GTC TAT GAG GAA CAA      684
111  Leu His His Asp Thr Asp Asp Val Thr Tyr Gln Val Tyr Glu Glu Gln
112  190                 195                 200                 205
113
114  GCA GTA TAT GAA CCT CTA GAA AAT GAA GGG ATA GAA ATC ACA GAA GTA      732
115  Ala Val Tyr Glu Pro Leu Glu Asn Glu Gly Ile Glu Ile Thr Glu Val
116                 210                 215                 220
117
118  ACT GCT CCC CCT GAG GAT AAT CCT GTA GAA GAT TCA CAG GTA ATT GTA      780
119  Thr Ala Pro Pro Glu Asp Asn Pro Val Glu Asp Ser Gln Val Ile Val
120                 225                 230                 235
121
122  GAA GAA GTA AGC ATT TTT CCT GTG GAA GAA CAG CAG GAA GTA CCA CCA      828
123  Glu Glu Val Ser Ile Phe Pro Val Glu Glu Gln Gln Glu Val Pro Pro
124          240                 245                 250
125
126  GAT ACT TAAAGCTTCA AAAAGACTGC CCCTACCACC ACAGGAGGAC CAGCCTAACC      884
127  Asp Thr
128         255
129
130  ATACGCTCCA AAAGATGGCT GTGATAGATC TTGTGAAGCA ATTACTGAGC AGATCAAGAT      944
131
132  CTTTGGGAAG GAACACTAAA GATGTTTTGA ATGAATTATA GTCCACTGGC ATTTTAGTGT     1004
133
134  ATTTTTTTTT CTTTTTAGAA ACACACATTT CTAAAAATGT CATGTTACAT TCCTGCATGT     1064
135
136  CCCTTTTGAT AGCATTAGTG GATCCATTGG ATTTCTTTTT TCTTTTTGTG AGACAGCTTT     1124
137
138  TAGTCTTACC TGAATTTATG TGTGTTTTTC CGACAGTGGT TAATAATTAT ATTGGTGATG     1184
139
140  TAGCAGCAAT TGTGTTGGCA GGGTTTTCAT ATATTATTAG TAATTAACAC TAACTGTTGG     1244
141
142  ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAGCT ATTAAGAGTA CTTTGTGTTA     1304
143
144  GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC     1364
145
146  CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTCAG ATTAACACTT     1424
147
148  TTGAAACCTT TGTAGCTTTT AGCTGATTAA TTAGAAAAAT TAATATTTCA GTGAAAGTTT     1484
149
150  TAAATTATCA TTTATTTATT TTTTTAAATG AGAGGGGAAA GCTGAAATTC CTTGTTAAGA     1544
151
152  CACAAGGAAA AAGAATGGCC CTACTATTAT CATGCAAAAA TGCTTTGTTG GCACCTCAGA     1604
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153
154    TTAATCATAT AATAGCTATA GTCTCTTCAG CATTTGTTTA AATTTTAGAA AACCTGTATA    1664
155
156    AATTACTGGT GCATAACTTA AAGATTATTC TGCCTTTGGC TAATTGAGTA ATTCCCCTCC    1724
157
158    AGCACTAGAG ACCGCTCAGT GCTCTTACTA GATGAACTCA GTAACGCCTT GAGCTGGGTT    1784
159
160    GATTGAGGAT GTGTGAAAAA GCTCACAGAG CCCGATGCCT GCTGCTATTT CACGGCAATG    1844
161
162    AGCCTTTTTC TTTCTACACT GAAGATTTTC TTCTTATTTA ATGTGGTTTA TTTTGGGCTC    1904
163
164    AGAAATAATT GCTCTGTTGA AAATAATCCT TTGTCAGAAA AGAAGGTAGC TACCACATCA    1964
165
166    TTTTGAAAGG ACCATGAGCA ACTATAAGCA AAGCCATAAG AAGTGGTTTG ATCGATATAT    2024
167
168    TAGGGGTAGC TCTTGATTTT GTTAACATTA AGATAAGGTG ACTTTTTCCC CCTGCTTTTA    2084
169
170    GGATTAAAAT CAAAGATACT TCTATATTTT TATCACTATA GATCATAGTT ATTATACAAT    2144
171
172    GTAGTGAGTC CTGCATGGGT ACTCGATGTG TAATGAAACC TGAAATAATA ATAAGATAAT    2204
173
174    AAGAAAAGCA ATAATTTTCT AAAGCTGTGC TGTCGGTGAT ACAGAGATGA TACTCAAATT    2264
175
176    ATAATAAAAC TCTTCATTTT GTGAATTATA GAAGCTACTT TTTATAAAGC CATATTTTTT    2324
177
178    TAGGGAAACT AAGGAGTGAC ATAGAACTGA TGAATGAGTA AAAGTAAGTT TTGCTGGATT    2384
179
180    TTTGTAGAAC TCTGGACGTT GAGGATTCAT TATGCTGTGG TTAACTTTAA ATATTTTT    2442
181
182
183    (2) INFORMATION FOR SEQ ID NO:2:
184
185            (i) SEQUENCE CHARACTERISTICS:
186                    (A) LENGTH: 255 amino acids
187                    (B) TYPE: amino acid
188                    (D) TOPOLOGY: linear
189
190            (ii) MOLECULE TYPE: protein
191
192            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
193
194    Met Val Ile Ala Leu Leu Gly Val Trp Thr Ser Val Ala Val Val Trp
195     1               5                  10                  15
196
197    Phe Asp Leu Val Asp Tyr Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr
198                20                  25                  30
199
200    Asp Ala Asp Gly Asp Gly Asp Phe Asp Val Asp Asp Ala Lys Val Leu
201                35                  40                  45
202
203    Leu Gly Leu Lys Glu Arg Ser Thr Ser Glu Pro Ala Val Pro Pro Glu
204        50                  55                  60
205
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```
206   Glu Ala Glu Pro His Thr Glu Pro Glu Glu Gln Val Pro Val Glu Ala
207    65              70              75              80
208
209   Glu Pro Gln Asn Ile Glu Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu
210                85              90                  95
211
212   Leu His Glu Met Val His Ala Glu His Val Glu Gly Glu Asp Leu Gln
213                100             105             110
214
215   Gln Glu Asp Gly Pro Thr Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe
216        115             120             125
217
218   Leu Met Ala Thr Asp Val Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu
219        130             135             140
220
221   Val Ser His Glu Glu Thr Glu His Ser Tyr His Val Glu Glu Thr Val
222   145             150             155             160
223
224   Ser Gln Asp Cys Asn Gln Asp Met Glu Glu Met Met Ser Glu Gln Glu
225                165             170             175
226
227   Asn Pro Asp Ser Ser Glu Pro Val Val Glu Asp Glu Arg Leu His His
228                180             185             190
229
230   Asp Thr Asp Asp Val Thr Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr
231        195             200             205
232
233   Glu Pro Leu Glu Asn Glu Gly Ile Glu Ile Thr Glu Val Thr Ala Pro
234        210             215             220
235
236   Pro Glu Asp Asn Pro Val Glu Asp Ser Gln Val Ile Val Glu Glu Val
237   225             230             235             240
238
239   Ser Ile Phe Pro Val Glu Glu Gln Gln Glu Val Pro Pro Asp Thr
240                245             250             255
241
242   (2) INFORMATION FOR SEQ ID NO:3:
243
244        (i) SEQUENCE CHARACTERISTICS:
245             (A) LENGTH: 28 amino acids
246             (B) TYPE: amino acid
247             (C) STRANDEDNESS:
248             (D) TOPOLOGY: linear
249
250        (ii) MOLECULE TYPE: peptide
251
252
253
254
255        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
256
257        Val Lys Lys Ala Phe Ala Ile Ile Asp Gln Asp Lys Ser Gly Phe Ile
258        1               5               10                  15
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/040,485*

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